

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:40:32 : Search time 18 2143 Seconds
(without alignments)
56.562 Million cell updates/sec

Title: US-09-856-070-26
Perfect score 28
Sequence: 1 Q9H45

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organello:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protein:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	28	100.0	106	4	Q9H4N4	Q9H4N4 homo sapien
2	28	100.0	125	5	Q45212	Q45212 bradylab
3	28	100.0	130	16	Q9K660	Q9K660 bacillus ha
4	28	100.0	156	16	Q9K011	Q9K011 bacillus ha
5	28	100.0	171	2	Q50138	Q50138 ruminocecu
6	28	100.0	179	5	Q95P73	Q95P73 haematobia
7	28	100.0	263	16	Q97N02	Q97N02 streptococ
8	28	100.0	260	1	Q97F00	Q97F00 streptococ
9	28	100.0	315	13	Q03292	Q03292 xenopus lac
10	28	100.0	361	16	Q97A44	Q97A44 streptococ
11	28	100.0	370	12	Q9P217	Q9P217 xestia c-ni
12	28	100.0	376	5	Q555W7	Q555W7 caenorhabdi
13	28	100.0	400	5	Q9VFC9	Q9VFC9 drosophila
14	28	100.0	404	5	Q8T0T3	Q8T0T3 drosophila
15	28	100.0	406	11	Q90TK3	Q90TK3 rattus norv
16	28	100.0	443	16	Q24532	Q24532 volvox cart

ALIGNMENTS

RESULT 1

Q9H4N4
ID Q9H4N4: PRELIMINARY; PRT; 106 AA.
AC Q9H4N4:
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Clone Q9H4N4 mRNA sequence.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95567227; PubMed=8513474;
FA Andersson B., Wentland M.A., Kitzfronke J.Y., Liu W., Gibbs K.A.;
PT "A 'double adaptor' method for improved shotgun library
PT construction";
RL Anal. Biochem. 236:107-113(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97264341; PubMed=9110174;
FA Yu W., Anderson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
FA Poirre J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
ET "Large scale cccatation cDNA sequencing.";
RI Genome Res. 7:353-358(1997)
RN [3]
RP SEQUENCE FROM N.A.
FA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
FA Macgregor J.F.;
RL S. Smith (J. Mol. Biol. 2000) in the EMBL/GenBank/TrEMBL databases.
OR EMBL, AY071145, AAC02031, 1;
SQ SEQUENCE 106 AA; 13211 MW; RCAG5559AG2000DE25 CRC64;

Query Match 100.0% Score 28; DB 4; Length 106;

Best Local Similarity 100.0%; Pred. No. 50; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q9 1 Q9H45

Query Match: 100.00; Score: 28; DB 2; Length 171;
Best Local Similarity 100.00; Pred. No. 1e-02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
|||||

Db 71 QDYE 75

RESULT 6

Q95P73 PRELIMINARY: PRT: 179 AA.

AC Q95P73; (1-DEC-2001 (TrEMBLrel. 19, Created))

DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Thrombostasin (Fragment).

OS Haematobia irritans (horn fly).

OC Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;

OC Pterygota; Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha;

OC Muscidae; Muscidae; Haematobia.

OX NCBI_TaxID=7368;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-SALIVARY GLAND;

RA Zhang D., Cupp M.S., Cupp F.W.

RT "thrombostasin: a novel anti-thrombin protein purified from horn fly saliva.";

RL Insect Biochem Mol Biol 0-0-0(2001)

FT EMBL: AF260078; AA660131;

FT NON_TER 1

SQ SEQUENCE 179 AA, 19910 MW, 46710ABRAIAIAKHA CRG64.

Query Match 100.0%; Score 28; ID 5; Length 179;
Best Local Similarity 100.0%; Pred. No. 1 to 62.

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
|||||

Db 87 QDYE 91

RESULT 7

Q97NV2 PRELIMINARY: PRT: 253 AA.

AC Q97NV2; (1-OCT-2001 (TrEMBLrel. 13, Created))

DI 01-OCT-2001 (TrEMBLrel. 13, Last sequence update)

DI 01-OCT-2001 (TrEMBLrel. 13, Last annotation update)

DE Oxidoreductase, short chain dehydrogenase/reductase family.

GN SP1909.

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;

OC Streptococcaceae; Streptococcus.

OX NCBI_TaxID=1313;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-TIGR4;

RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.P., Durkin S., Heidelberg J., DeBoy P.T., Haft D.H., Dodson P.J., Peterson A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.B., Umayam L.A., White O., Salzberg S.L., Lewis M.F., Padine B., Holtzapple E., Khouri H., Wolf A.M., Interback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Anquilli S., Dickinson T., Hickey E.K., Holt I.E., Lolait S.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";

RL Science 293:498-506(2001).

DF EMBL: AE007482; AA750781;

DB TIGR: SP1909;

DR InterPro: IPR002198; ADH_short

DR Pfam: PF00106; adh_short; 1.

DR PRINTS: PR00080; SDRFAMILY.

HP PROSITE: PS00061; ADH_SHORT: UNKNOWN_1.

KW Complete proteome.

SQ SEQUENCE 253 AA; 27455 MW; F6B2F1753C57181D CRG64;

Query Match 100.0%; Score 28; ID 16; Length 253;
Best Local Similarity 100.0%; Pred. No. 1 to 102.

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
|||||

Db 99 QDYE 103

RESULT 8

Q9F700 PRELIMINARY: PRT: 260 AA.

AC Q9F700; (1-MAR-2001 (TrEMBLrel. 16, Created))

DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Putative oxidoreductase.

OS Streptococcus thermophilus.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;

OC Streptococcaceae; Streptococcus.

OX NCBI_TaxID=1308;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE: 20455572; PubMed 19983327;

RA Lucchini S., Sidoti J., Brusow H.

RT "Broad-range bacteriophage resistance in Streptococcus thermophilus by insertional mutagenesis.";

RL Virology 275:257-277(2000).

CC -1- SIMILARITY: REFIONS TO THE SH-PT-HAIN PEPYD-RENASES/PEPTIDASES (SDR) FAMILY.

DP EMBL: AF288038; AA322016.1;

DR InterPro: IPR002198; ADH_short.

DR Pfam: PF00106; adh_short; 1.

DR PRINTS: PR00080; SDRFAMILY.

DR PROSITE: PS00061; ADH_SHORT: UNKNOWN_1.

KW Oxidoreductase.

SQ SEQUENCE 260 AA; 29120 MW; BD45DFBCEB12CB21 CRG64;

Query Match 100.0%; Score 28; ID 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 1 to 102.

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
|||||

Db 104 QDYE 108

RESULT 9

Q03292 PRELIMINARY: PRT: 315 AA.

AC Q03292; (1-NOV-1996 (TrEMBLrel. 01, Created))

DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Animal 4 (Xian4).

OS Xenopus laevis (African clawed frog).

OC Pterygota, Metazoa, Chordata, Grenata, Vertebrata, Batrachostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE: 9318758; PubMed=1284029;

RA Reddy H.A., Kloc M., Ptkin L.D.

RT "The cloning and characterization of a localized maternal transcript in Xenopus laevis whose zygotic counterpart is detected in the CNS.";

PL Mech Dev 39:141-150(1992)

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

DR EMBL: M94969; AAA73357.1; -.

```

DR HSSP: P27986; IPHT.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00019; SH3; 1.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRODOM: PD000066; SH3; 1.
DR SMART: SM00426; SH3; 1.
DR PROSITE: PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 315 AA; 34257 MW; A517E2FC0AF017AF CRC64;

Query Match 100.0%; Score 28; DB 13; Length 315;
Best local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
DB 226 QDYE 230

RESULT 10
Q97RA4 PRELIMINARY; PRT; 361 AA.
AC Q97RA4;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DE Hypothetical protein SP0921.
CN SP0921.
OS Streptococcus pneumoniae
OC Bacteria; Firmicutes; Bacillus/Clostridium group, Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TIGR4;
RX MEDLINE-21357209; PubMed-11463916;
RA Terrellin H., Nelson K.E., Paulsen I.I., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Petersen J.P.,
RA Mayhew I.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Anglucci S., Dickson T., Hickey E.K.,
RA Holt I.E., Lolius B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RA "Complete genome sequence of a virulent isolate of Streptococcus
RA pneumoniae."
RT Science 293:498-506(2001).
DR EMBL: AE007397; AAK75045.1;
DR TIGR: SP0921;
KW Hypothetical protein, Complete proteome.
SQ SEQUENCE 361 AA; 40341 MW; HPEEAPB3F0773250 CRC64;

Query Match 100.0%; Score 28; DB 16; Length 361;
Best local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
DB 124 QDYE 127

RESULT 11
Q9PZ17 PRELIMINARY; PRT; 370 AA.
AC Q9PZ17;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OMF26.
OS Xestia c-nigrum granulosis virus (XnGV) (Xestia c-nigrum
OS granulovirus).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus
OX NCBI_TaxID=51677;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99434230; PubMed-10502508;
RA Hayakawa I., Ko R., Okano K., Scong S.L., Goto C., Maeda S.;
RT "Sequence analysis of the Xestia c-nigrum granulovirus genome."
PL Virology 262:277-287(1999)
DR EMBL: AF162221; AAF05140.1;
SQ SEQUENCE 370 AA; 42913 MW; 4EFD1A45F050CE84 CRC64;

Query Match 100.0%; Score 28; DB 12; Length 470;
Best local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
DB 151 QDYE 155

RESULT 12
Q95QW7 PRELIMINARY; PRT; 376 AA.
AC Q95QW7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DE Hypothetical 44.4 kDa protein.
CN C14F5.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Rhabditinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-99069613; PubMed-9851916;
RA None;
PT "Genome sequence of the nematode C. elegans, a platform for
PT investigating biology. The C. elegans Sequencing Consortium."
KL Science 282:2012-2018(1998).
KL [2]
RP SEQUENCE FROM N.A.
RC STRAIN BRISTOL N2;
RA Minx P.;
RT "The sequence of C. elegans cosmid C14F5."
RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission."
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: U29082; AAI02434.1;
KW Hypothetical protein.
SQ SEQUENCE 376 AA; 44436 MW; 53E3255B13C4A6CE CRC64;

Query Match 100.0%; Score 28; DB 5; Length 376;
Best local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDYE 5
DB 99 QDYE 103

RESULT 13
Q9VFC9 PRELIMINARY; PRT; 400 AA.
AC Q9VFC9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DE CG3987 protein.
GN CG3987.

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OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta.
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha.
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 PP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.F., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.P., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon P.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abul J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin B.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
 RA Borkova P., Botchan M.P., Bouck J., Brokstein P., Brotlier P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos R., Delecher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup I.E., Dowies M., Duan-Rocha S., Dunkov R.C., Dunn P.,
 RA Durbin K.T., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Gloddek A., Gong F., Guieril J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Hatvey P., Heiman T.J., Hernandez I.R., Hoepf J.,
 RA Hostin D., Houston K.A., Howland T.L., Wei M.-H., Ibeagwa E.,
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel R.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Lei Y., Levinsh T.C., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., Moperson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy R., Murphy J., Murny D.M., Nelson D.I.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pauley J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun F.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage J., Worley K.C., Wu D., Yang S., Yao D.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs K.A., Myers E.W., Rubin G.M., Venter J.
 RT "The genome sequence of Drosophila melanogaster."
 FI Science 287:2185-2195(2000)
 DR EMBL: AE004707. AAF51411
 DR FL:Base: FB00038292; GS3987
 SQ SEQUENCE 400 AA; 45634 MW; 3B7A8C55327B353C CRC64;

Query Match 100.0%; Score 28; DB 5; Length 400;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYEE 5
 DB 44 QYEE 48
 |||||

RESULT 14

Q8T0T3 PRELIMINARY; PPT: 404 AA
 AC Q8T0T3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE GH09123p.
 GN CG3987.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta.
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila

OX NCBI_TaxID=7227;
 RN (1)
 RE SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson I.,
 RA Champe M., Chavez C., Dorset V., Partan D., Frise E., George P.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.T.,
 RA Ninkovic J., Pavl-B.J., Paragas V., Park S., Phuanuavong S., Wan K.,
 RA Yu C., Lewis S.F., Rubin G.M., Celnik S.
 PL Submitted (06-2001) to the EMBL/GenBank/DBJ databases
 DR EMBL: AY069074; AAL39219.1;
 SQ SEQUENCE 404 AA; 46060 MW; 2E305852FEF9315R CRC64;
 Query Match 100.0%; Score 28; DB 5; Length 404;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYEE 5
 DB 48 QYEE 52
 |||||

RESULT 15

Q9JIK3 PRELIMINARY; PPT: 406 AA.
 IN Q9JIK3
 AC Q9JIK3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Regulator of steroidogenic factor 1 (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclerotognathi; Muridae; Rattus.
 ON NCBI_TaxID=10116;
 PN (1)
 PP SEQUENCE FROM N.A.
 RC STRAIN=SPAGNE-DANLEY; TISSUE=OVARY;
 RX MEDLINE=20581305; PubMed=11145740;
 RA Ou Q., Mouillet J.-F., Yan X., Dorn C., Crawford P.A., Sadovsky Y.;
 RT "The hP40 Box Protein DP103 Is a Regulator of Steroidogenic Factor-1";
 PL Mol. Endocrinol. 15:69-74(2001)
 DR EMBL: AF220455; AAF76302.1;
 FT NON-ITER 1
 SQ SEQUENCE 406 AA; 45591 MW; 40D02608498B807 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 406;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYEE 5
 DB 353 QYEE 357
 |||||

Search completed: January 16, 2003, 16:55:49
 Job time : 20.2143 secs

